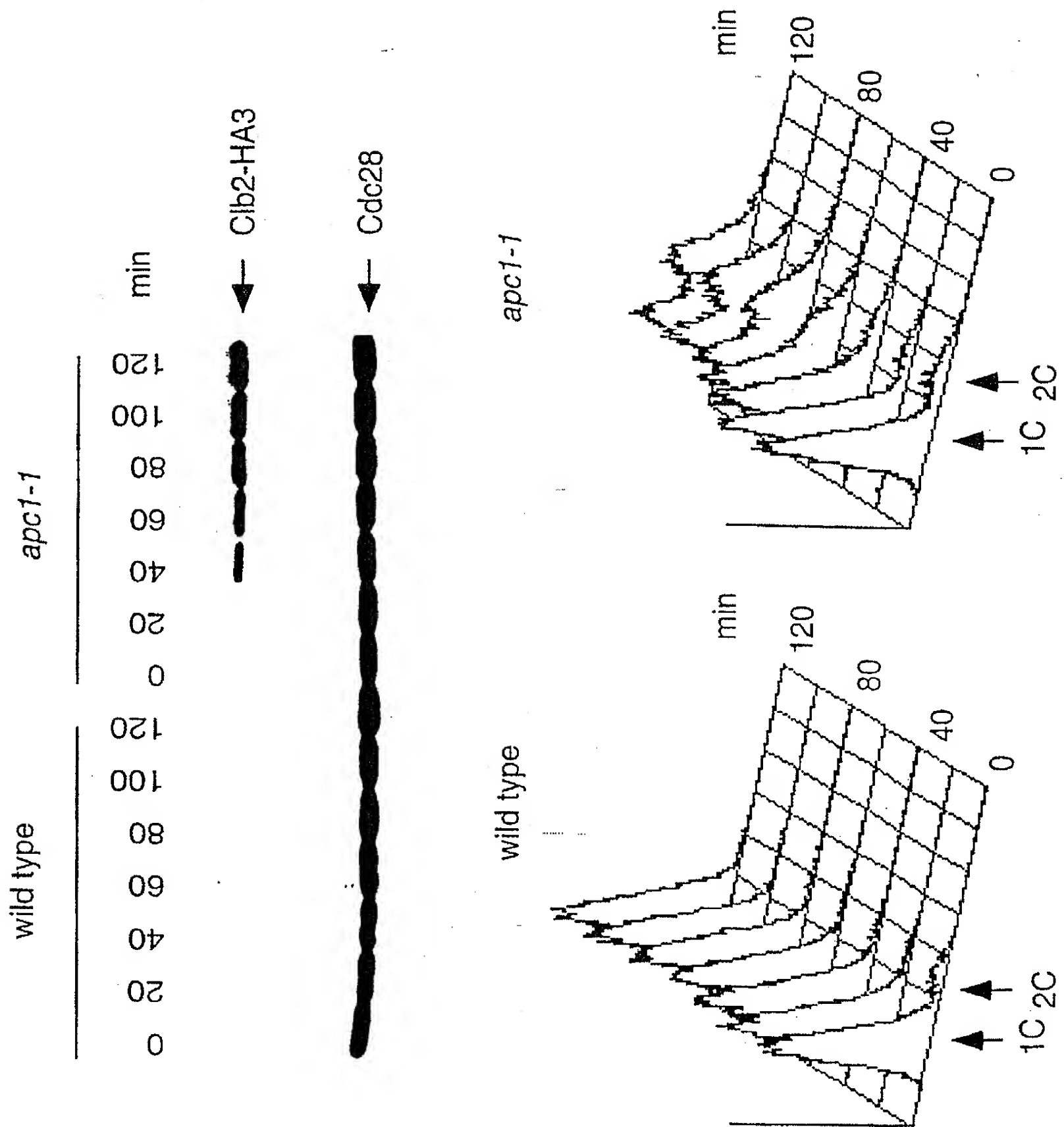
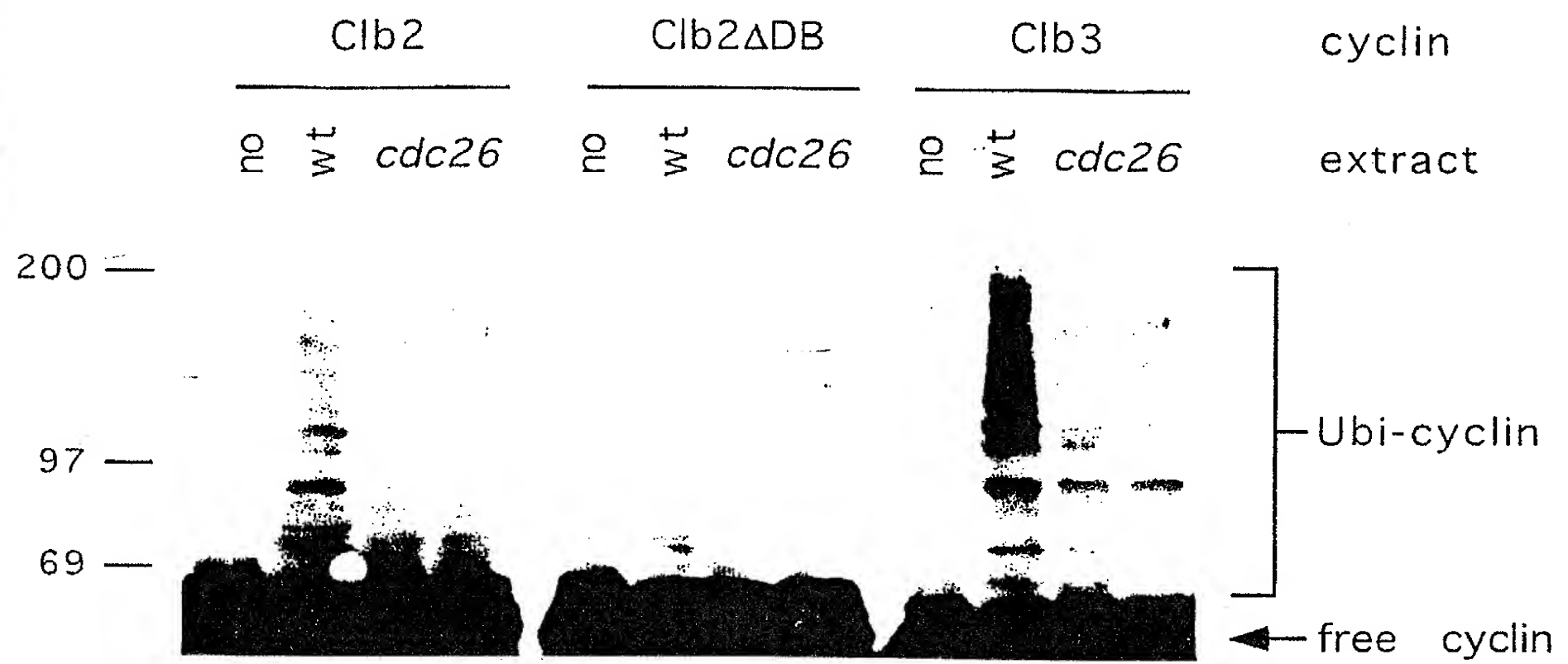


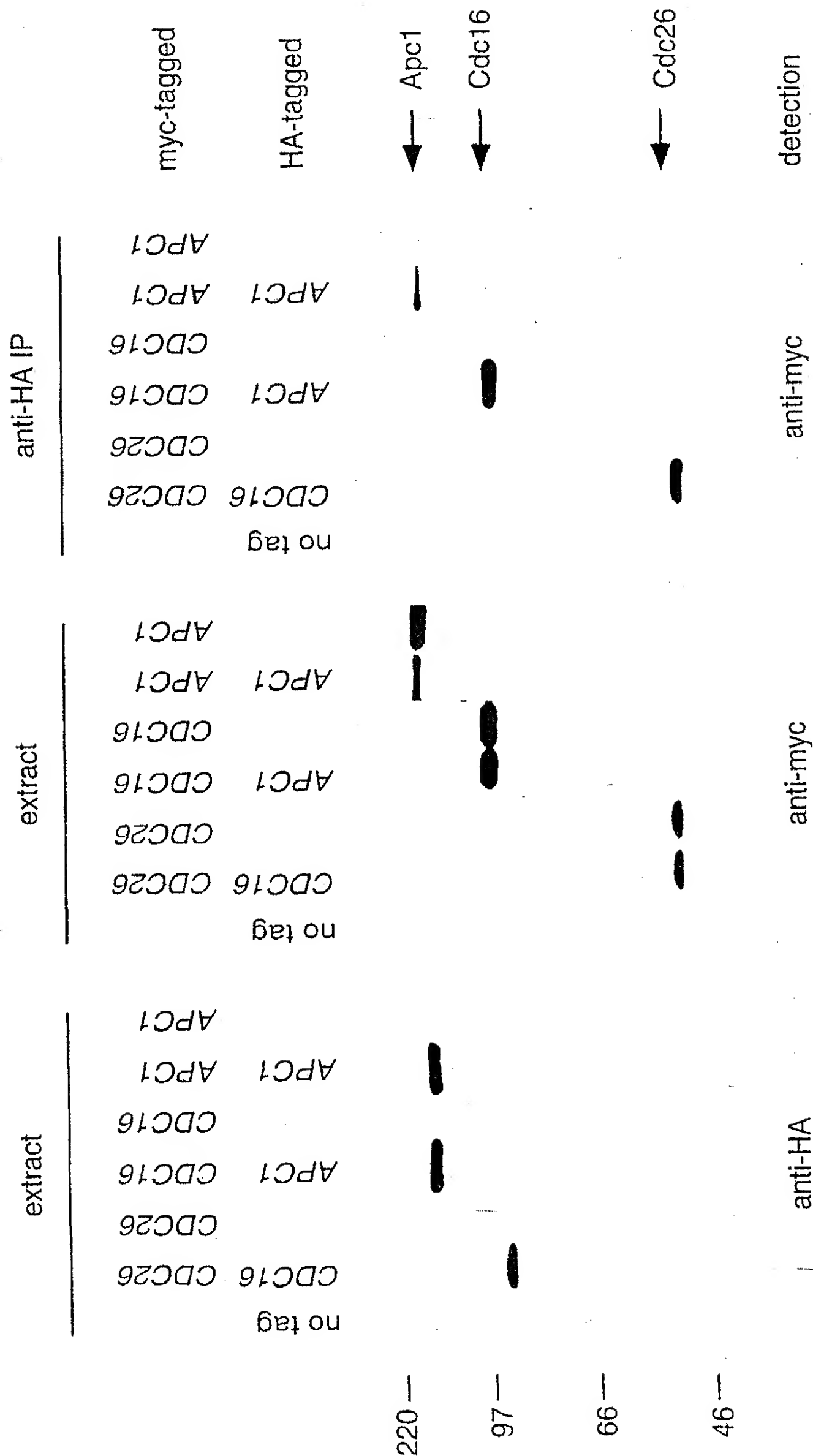
1/22  
Fig. 1A



2/22  
Fig.1B

Western blot analysis showing the ubiquitination of cyclin in *Clb2*, *Clb2 $\Delta$ DB*, and *Clb3* strains. The blot is probed with anti-cyclin antibody. Molecular weight markers are indicated on the left (200, 97, 69 kDa). On the right, a bracket indicates the region of ubiquitinated cyclin (Ubi-cyclin) and an arrow points to the free cyclin band. The lanes are labeled: *Clb2* (no, wt, *apc1*), *Clb2 $\Delta$ DB* (no, wt, *apc1*), and *Clb3* (no, wt, *apc1*). The *Clb2* and *Clb3* strains show a prominent Ubi-cyclin band in the wt lanes, which is reduced in the *apc1* mutant. The *Clb2 $\Delta$ DB* strain shows a prominent Ubi-cyclin band in the wt lane, which is reduced in the *apc1* mutant. The *Clb2* and *Clb3* strains show a prominent Ubi-cyclin band in the wt lanes, which is reduced in the *apc1* mutant. The *Clb2 $\Delta$ DB* strain shows a prominent Ubi-cyclin band in the wt lane, which is reduced in the *apc1* mutant.

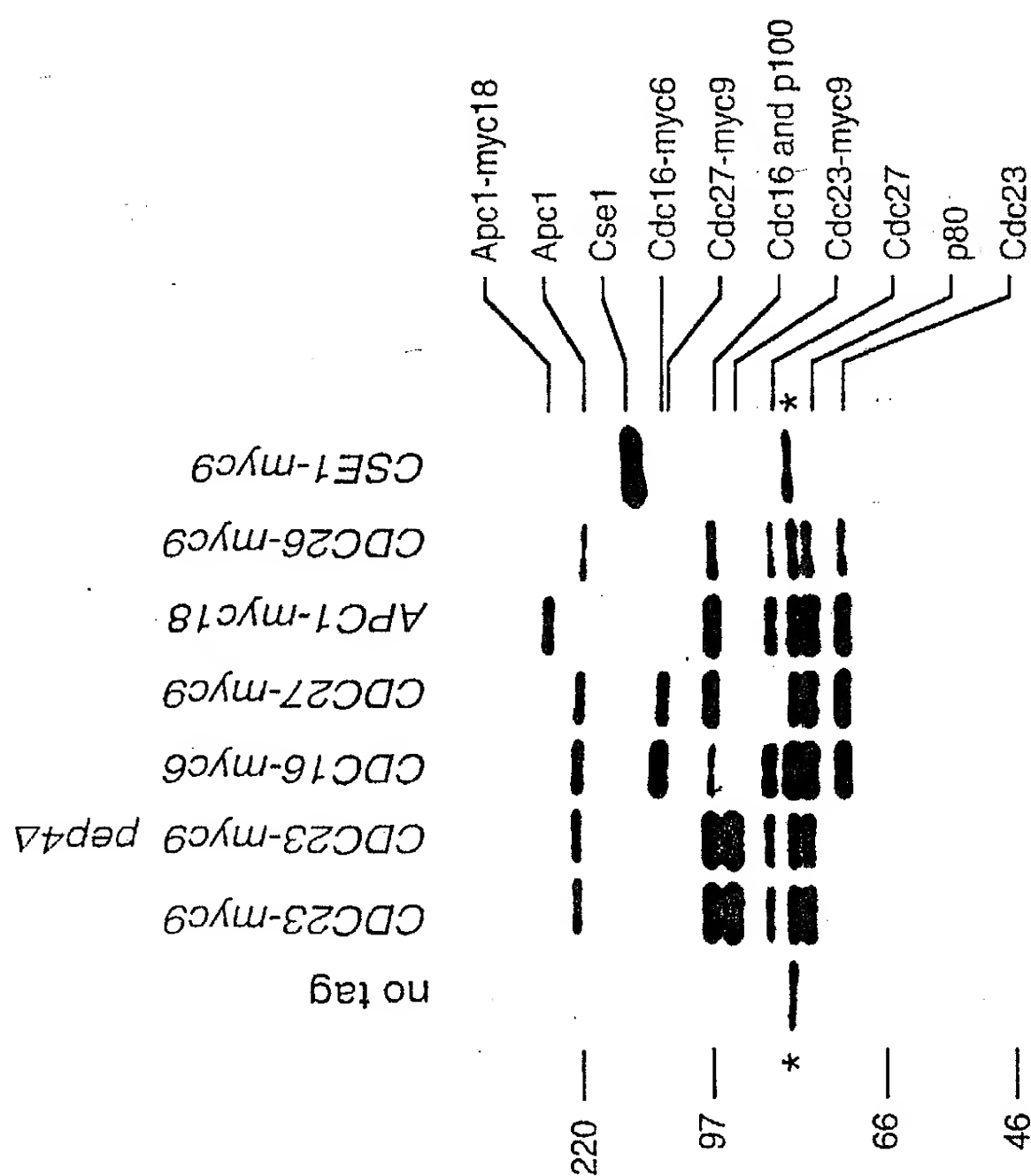
4/22  
Fig.2A



APC1, CDC26, Cdc16  
BY CLASS  
CRAFTED

482030-0000000000

5/22  
Fig. 2B

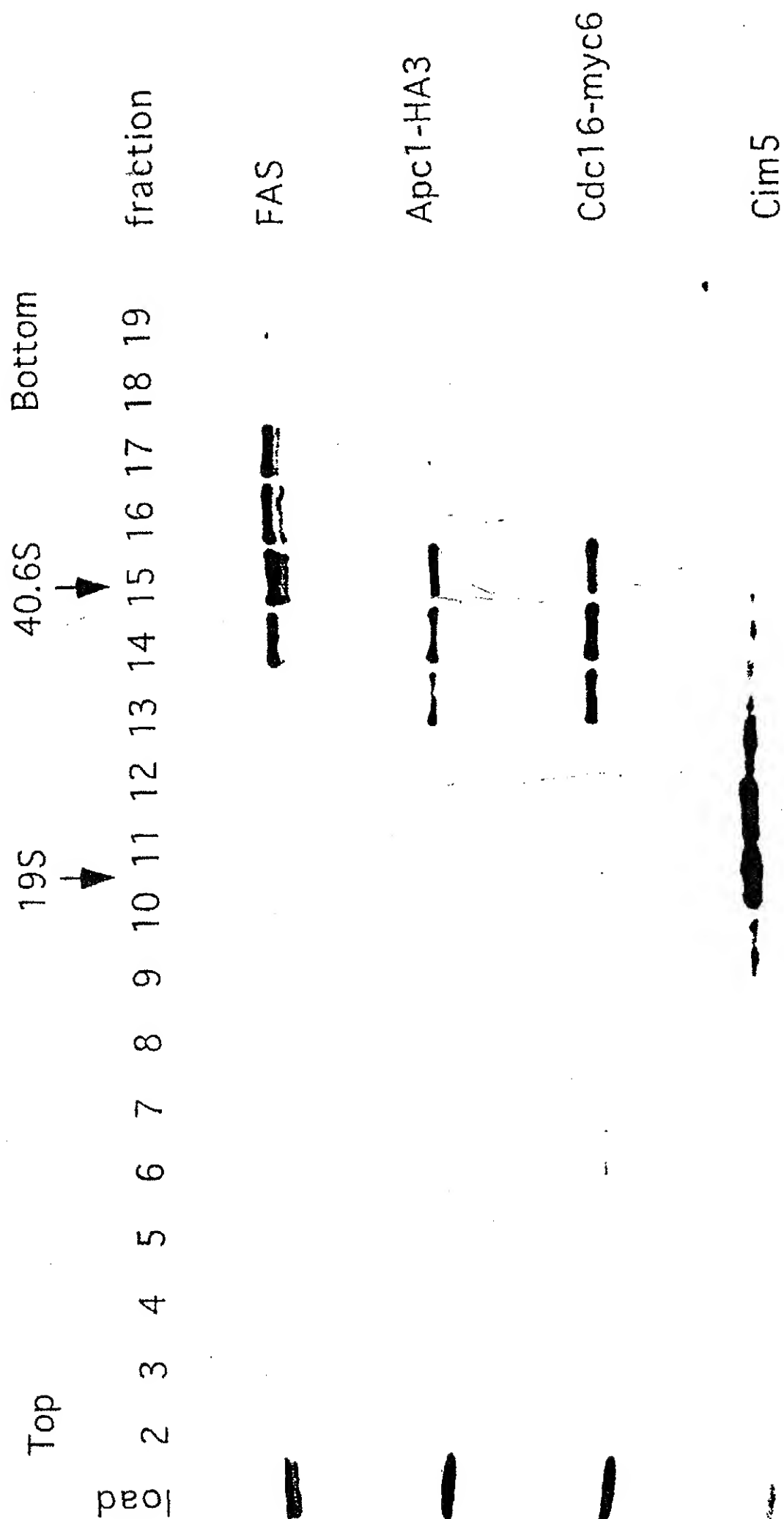


APPROVED O.G. FILE  
BY  
DRAFTING

604393-604393-604393

6/22  
Fig. 3A

0.3 FIG.  
GLASS SUBCLASS  
BY  
DATE



Top	19S	40.6S	Bottom
1	2	3	4
5	6	7	8
9	10	11	12
13	14	15	16
17	18	19	20

fraction

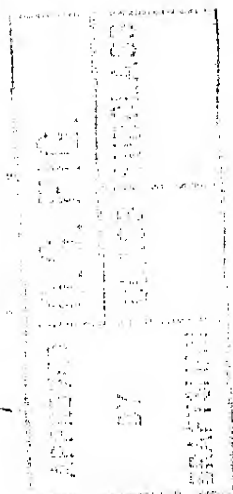
FAS

Cse1-myc9

Cdc16-HA3

Cdc26-myc9

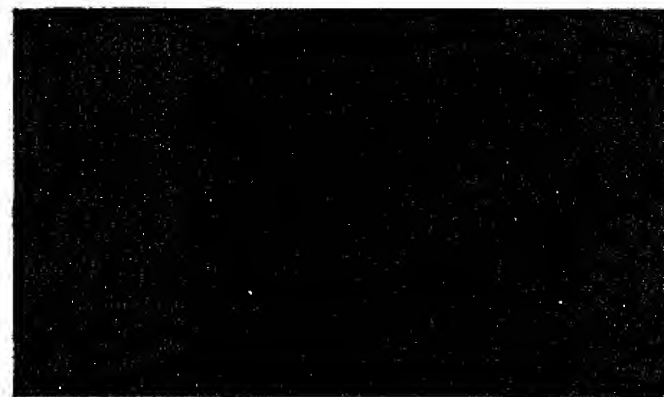
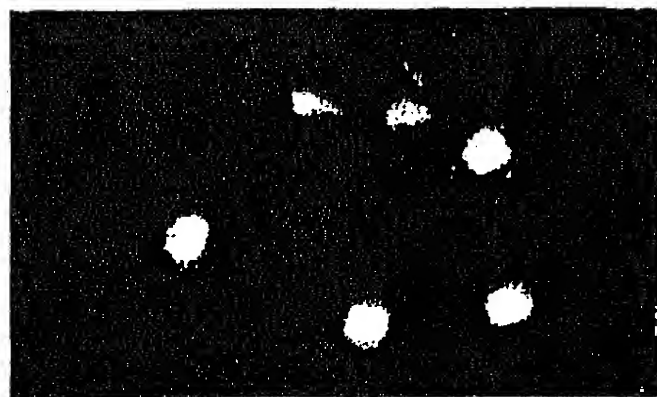
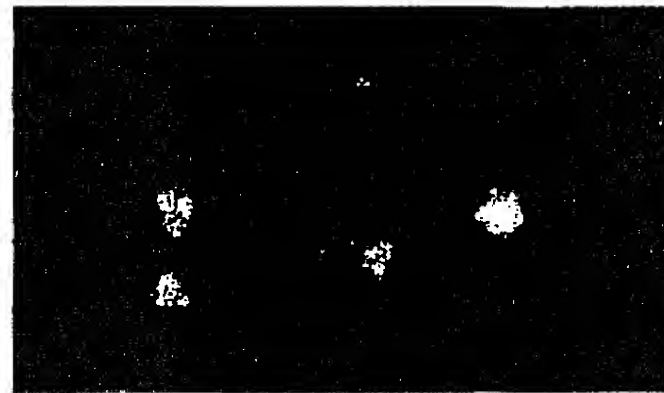
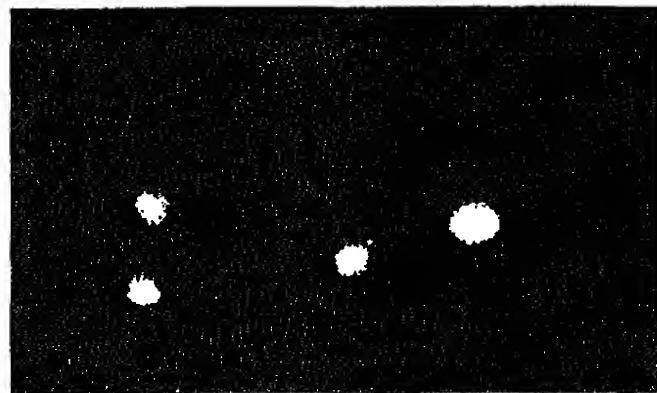
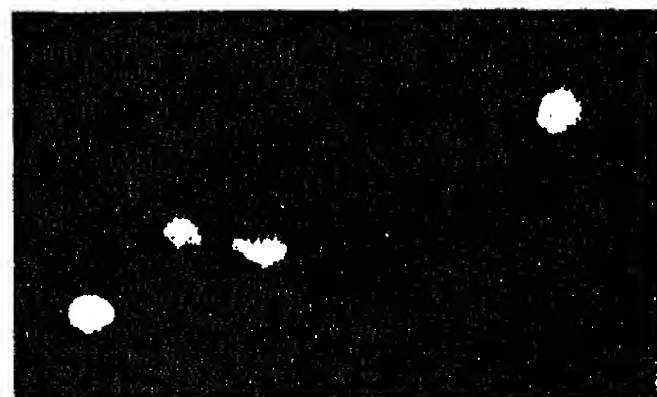
Cim5

8/22  
Fig. 4

DAPI

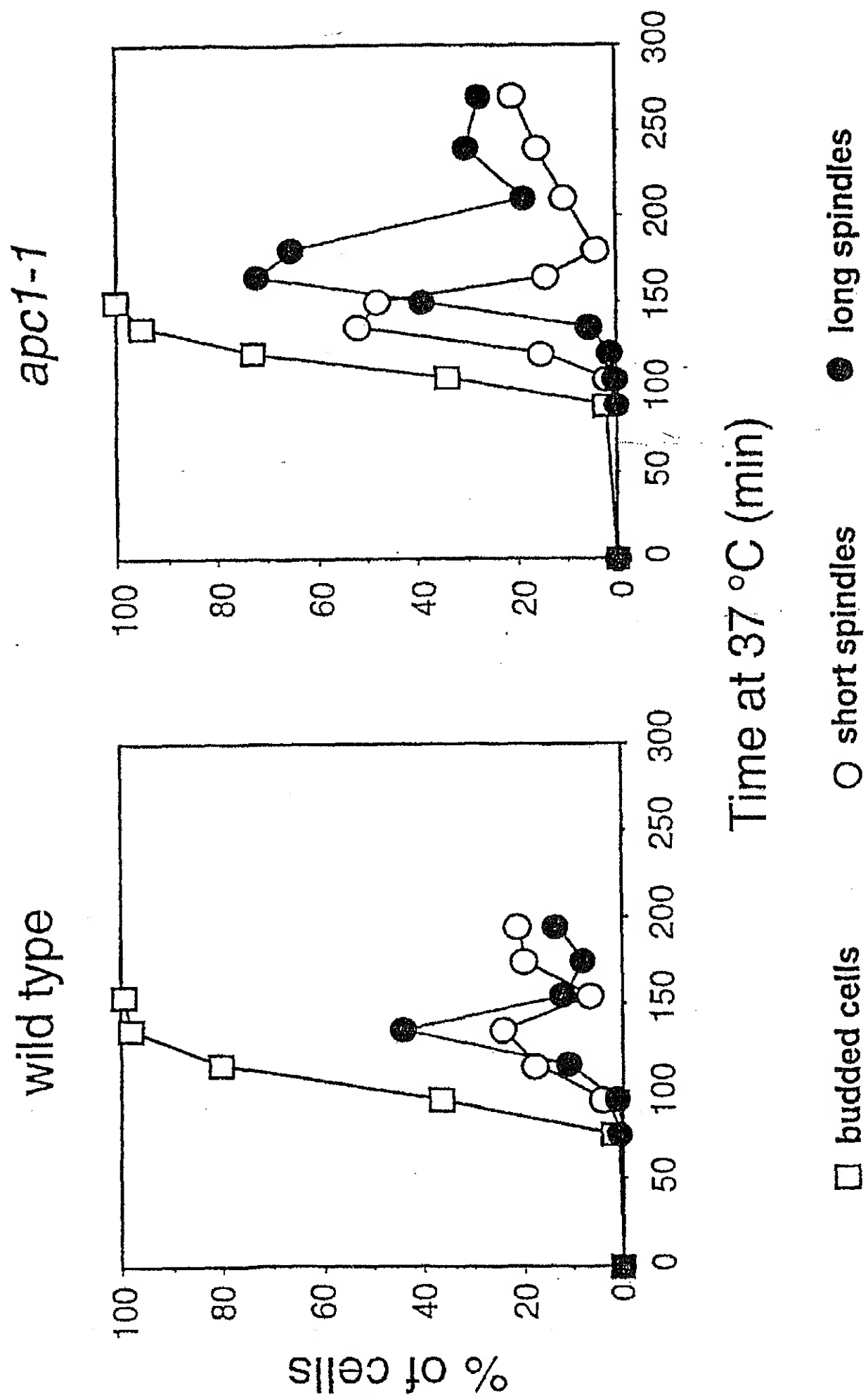
anti-myc

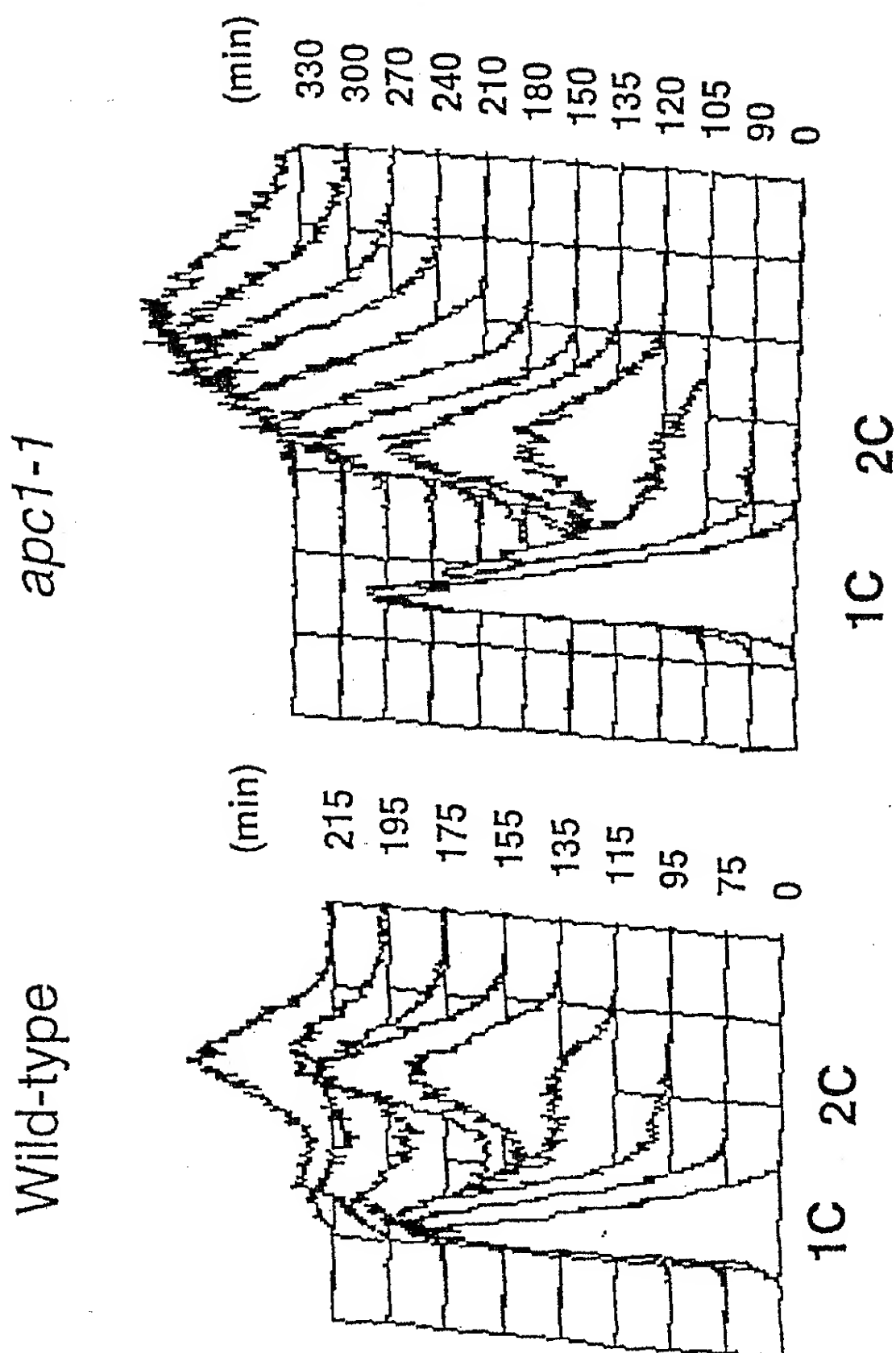
no myc

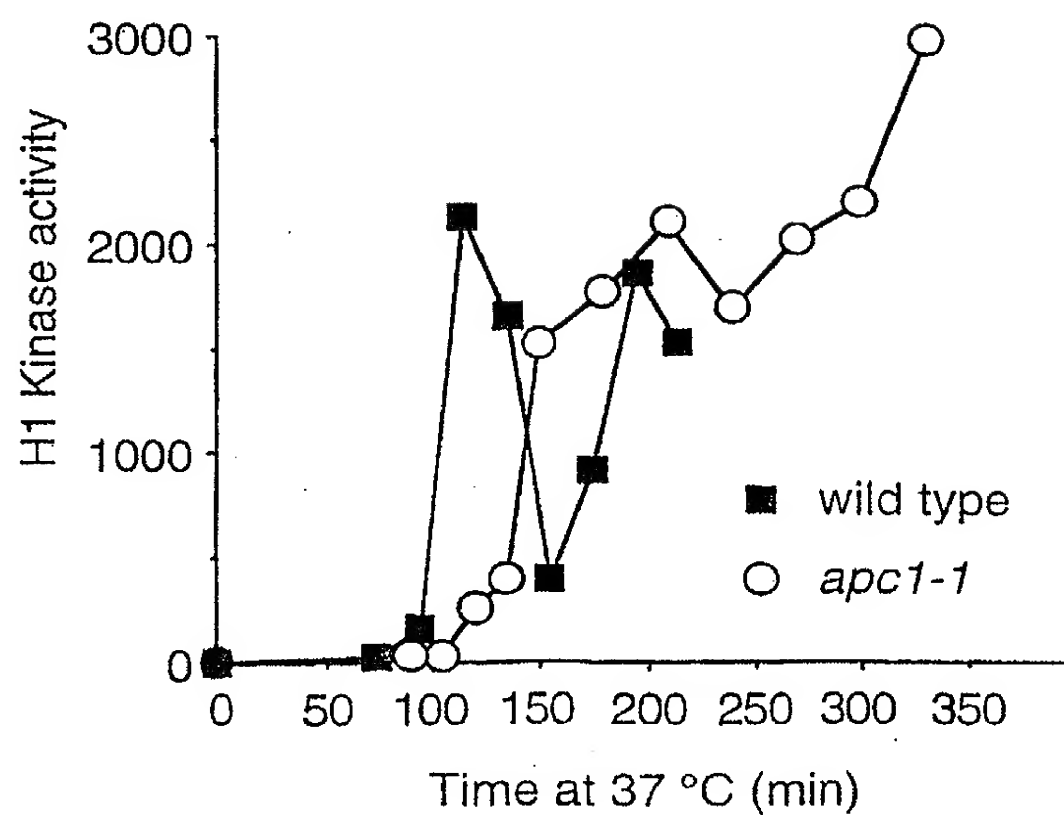
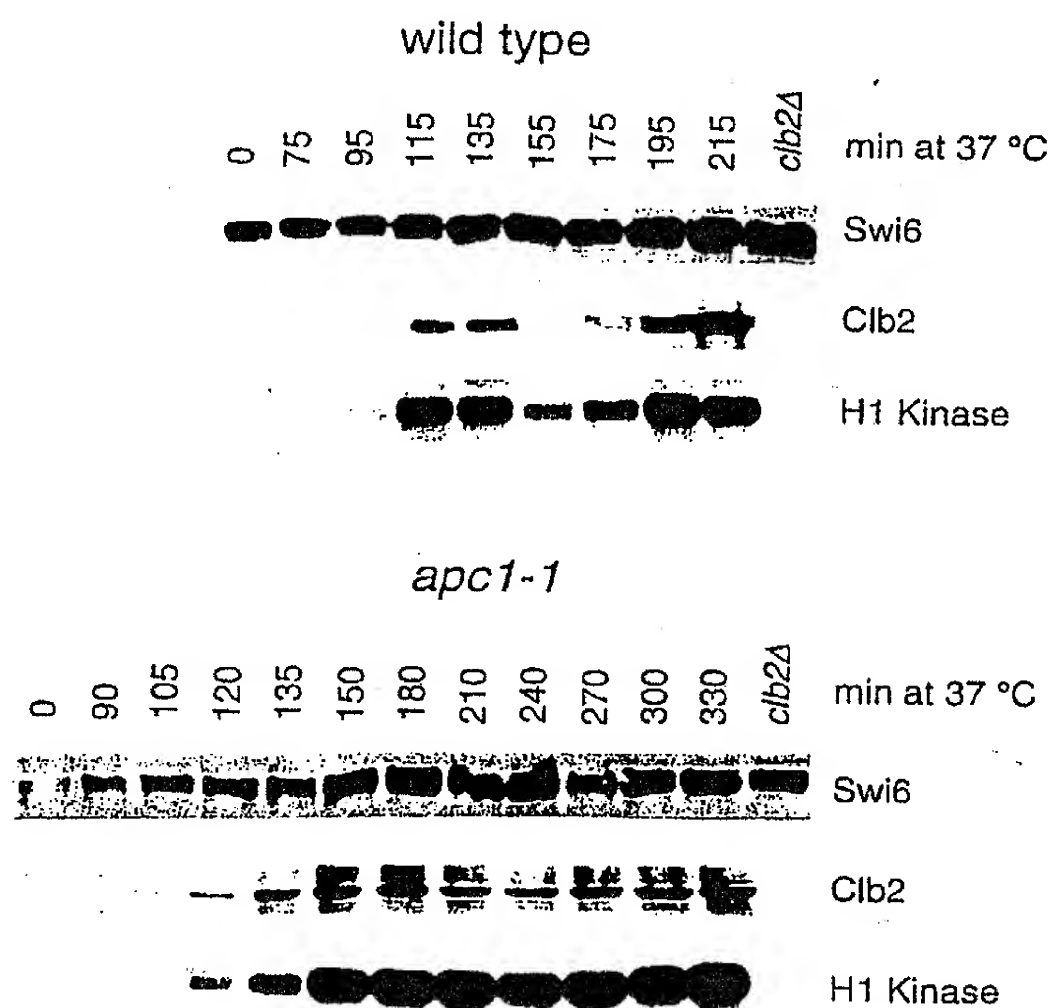
*CDC16-  
myc6**CDC26-  
myc9**APC1-  
myc18*

09/308109

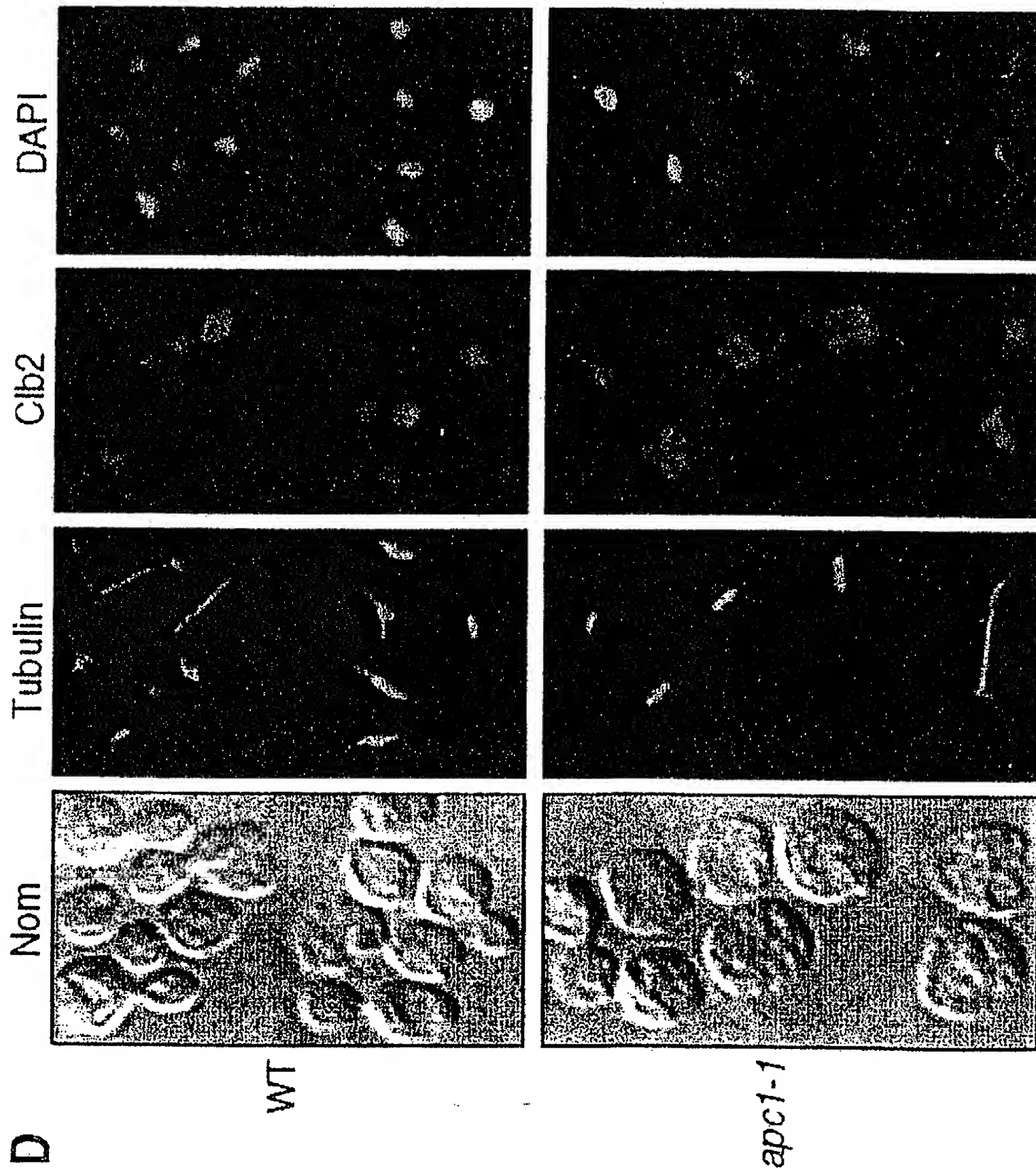


9/22  
Fig. 5A

10/22  
Fig. 5B

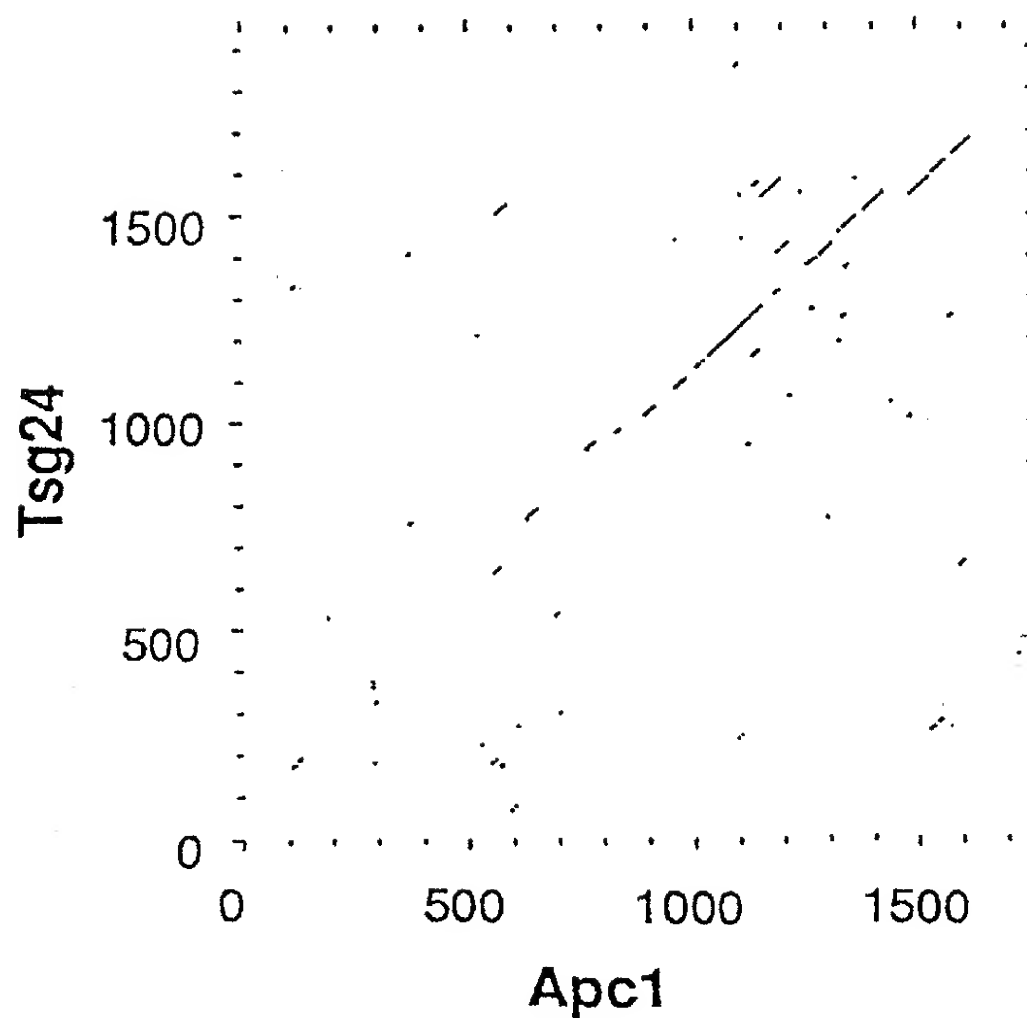
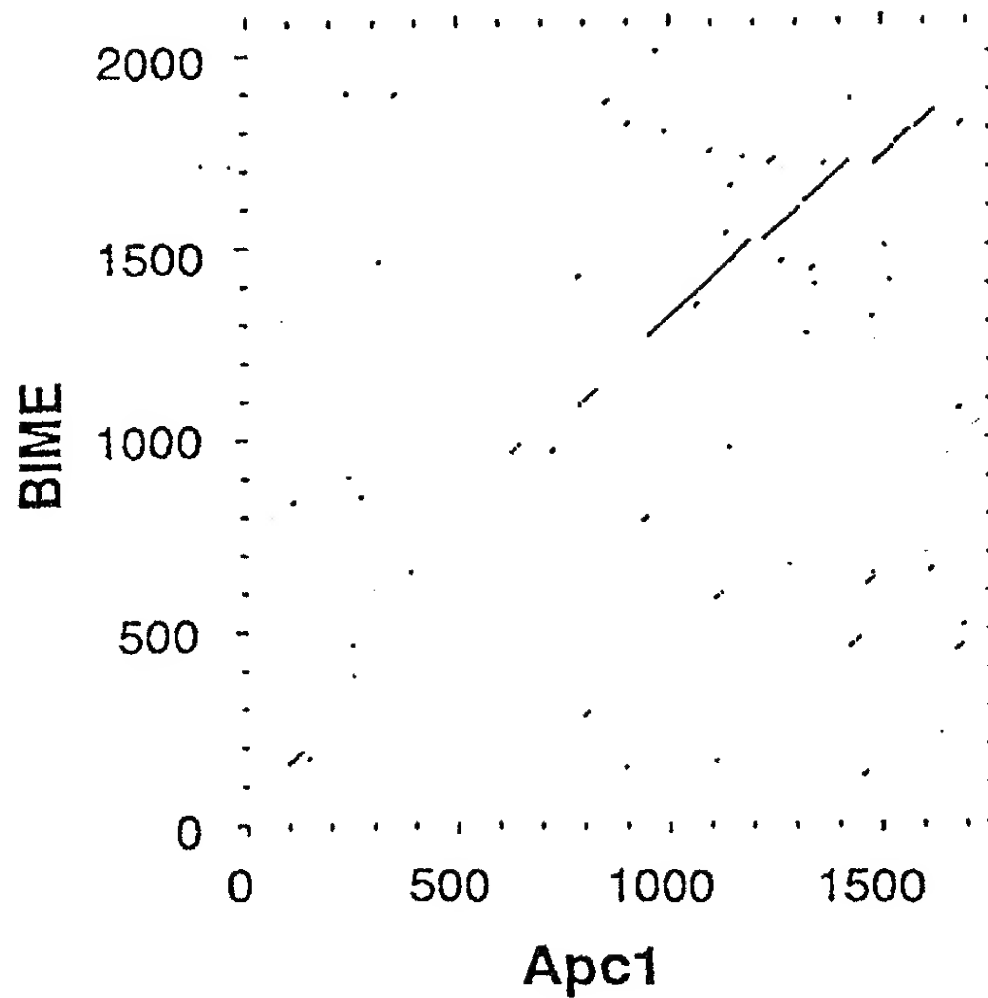
11/22  
Fig. 5C

12/22  
Fig. 5D



602090-00120000  
O.G. FIG.  
CLASS: UNCLASS  
DRAFTSMAN

13/22  
Fig. 6A



14/22  
Fig. 6B

apc1 AGDIFSEDKRFTHVVSLLAYRPTKTKQFFT.TKTEYAQIQAQKRYFAKIMALRTCTNGVG 960  
bime . . . LIFREDKRFIEAARLLNQSKAPAAECHPEPEWTDSDLEAQKRYFAKIMALRTCTNGVG 1274  
tsg24 . . . LIWSEDLRVQHVRRLLOSAQFVRVNVVQYPELSDEHFEIEERENRLLQLCQRTMALPVG 1083  
Consensus - - LIFSEDKRF - HV - RLL - - - - P - - - - - PE - - D - - - - LE - KE - - - - - LRT - - - - - PVG 1366

apc1 WGAWAYATEKPISTQKRWVIOPLNLSVFE. . . DDTKITVKAPEDIANDIVEWQGFHAGVSS 1018  
bime RAMLA FSGRLPLLTTERLPISFSLQCTMKPFSNVTTISADRASFH. . . EEKICWAFHNGVST 1332  
tsg24 RGMFTLFSYHPVPTTEPLDVRKLNLTGRAPPRNTTVDLNSGNIDVPPNMAWASPHNGVAA 1143  
Consensus RGM - A - - - - - P - - - - - TERLPIS - LNL - - - - - V - PP - N - T - - - - - A - - D - - - - - WA - PHNGVS - 1426

apc1 GLRISKKATGITCSVIAFNKPK. . . ELDAYHGGFLLGLGLNGHLKNDEEWHIYNLYSPRNT 1076  
bime GLAISXN SKGIDTSVILENKPO. . . ELTNRHAGFLLALGLNGHLRSIAKVVAFKYLTEKHT 1390  
tsg24 GLKIAPASQ. . . IDSAMIVVNRPKHAELANEYAGFLMALGLNGHLTKLATLNTHDYLTAKHE 1202  
Consensus GL - ISK - S - GID - SVI - ENKPK - - - - - EL - N - HAGFLLALGLNGHL - - - - - LA - W - I - - - - - YLTP - HT 1486

apc1 HISIGLLLCMSSSMKGSMDSKLIEVISVHLVAFLEPSGSSDLNIDLKLOTAGIIGMGNLYL 1136  
bime NTSIGLLLCGLSASVLTGMDTLVTRLLSVHVTMRMELPMGAAELNLSPLTOTAGIMGIGLYC 1450  
tsg24 NTSIGLLLCGLVSAAKLGTMDSITRLLSIHVPALEPPTSTELDVPHNVQVAAVVGIGLVQ 1262  
Consensus NTSIGLLLC - SAS - LGTMD - - - - - TRLLSVHV - A - LP - GS - ELN - - - - - OTAGI - GIGLY - 1546

apc1 NSRHHRMSDSIFAQLVSLNVIDEMVAD. . . EYRLAAGISLGLNLGAGGQTKLRKWD 1192  
bime NSQHHRMSEVMISEIENADQEEGSAATNDYLRNEGYRLAAGFALGFNLGKG. . . . . K 1502  
tsg24 GTHHRHTAEVLAEICRPPGPEMEYCTD. . . RESYSLAAGLALGMVCLGHG. . . . . S 1311  
Consensus NS - HHRMSEV - LAEI - - - - - E - E - - - - D - - - - - E - YRLAAG - ALG - INLG - G - - - - - S 1606

apc1 SLLGLCD. . . DLPEDEVHDSSEVQNVMYEDLTTKLLEIVTSTY. . . DVENDWTPENSQIGAVIA 1250  
bime DLKGRDMHIVERGLAVAVGT. . . . . KNYDLAHVLDORATAGATIA 1542  
tsg24 NLIGMSDLNVPEQLYQYMGVGHRRFQTGMHREKHKSPSYQIEGCDTINV. . . DVTCPGATIA 1370  
Consensus - L - GN - D - - - - - PE - LY - - - - - VG - - - - - - - - - - - K - YD - - - - - V - D - - - - - GATIA 1666

apc1 IMFLEFLSNFSGISNMELKVDLKEIEKANTNTRPELLNYREWASNMILUEFIGODLSFIMK 1310  
bime LAIIFMKTNDETTLAQKVDIPDTTVRFDYV. . . RPDLELLRLTLARHIIMDRIQACDEIFIG 1600  
tsg24 LAMIYLLKTNRSIAOWLRAPDTMYLDFV. . . RPEFLLRLTLARCLILVDDILPNSKVVDS 1428  
Consensus LA - IFLEKTN - - - - - IA - - - - - L - - - - - PDT - - - - - L - D - - - - - V - - - - - RPEULLRLTLAR - - - - - ILVD - - - - - I - - - - - N - - - - 1726

apc1 DV. . . . . DIGVKFSE. . . LNTDLLPIYYTHAGRI LAMGI RFASTGNLXIRNIAL 1355  
bime SLBEVYR. . . RRYRITGVRRLKSNOMPF. . . . . FNIIAGLCFALGLRFAGSPDPTVRDIL 1652  
tsg24 NVPQIIRENSISLSETELPCSEDLNLEELLSQAHVYIIAGACLSLGFREFAGSENLISAFSCL 1488  
Consensus - VE - - - - - R - - - - - L - - - - - A - - - - - SED - - - - - L - T - - - - - YIIAG - CLALG - RFAGS - NL - - - - - R - IL 1786

apc1 LSLVDKELPLYQYEGKONLDFRITISVINVLNTNVTVVSLSHVNCASGDLEVLRRVXYLHE 1415  
bime LSYLDQFIRISRLPA. . . PNYDARLARNVSRHCQDVVALSLAAVMAGTGDLALFRLRLSLH 1710  
tsg24 HKFAKDFEMNY. . . LSA. . . PN. . . ASVTGPYNLETCLSVL LSLAAVMAGSGNKKVLQLCRFLH 1543  
Consensus LS - - - - - D - - - - - LPA - PN - D - RI - - - - - C - - - - - VV - LSLAAVMAGSGDT - - - - - VLR - R - LH - 1846

apc1 VASGPYSOLFQEIIPSSKSDVSGVTQVTSNTNTPGNSDRERVDETAASLDDERSSSNGSDIS 1475  
bime . . . . . 1710  
tsg24 . . . . . 1543  
Consensus - - - - - 1906

apc1 DPTAYLEDKRDIDDHYGKFISTHUALGFLFLGSGQYALNTSTLESIAFLMSVLPYTTTP 1535  
bime . . . . . GRVDPDTFYGSHMAAHNAIGMLFLGGGSVYTLGTSNLAVASLIG. . . SLVPIEPTT 1762  
tsg24 . . . . . MKTCGEMNYGFHLAHHMALGLLFLGGGRYSLSSTSSSSIAALLC. . . ALYPHFAH 1595  
Consensus - - - - - K - D - D - - - - YG - H - A - HNALG - LFLGGG - Y - L - TSNL - - - - - AALLC - SLVP - EPT - 1966

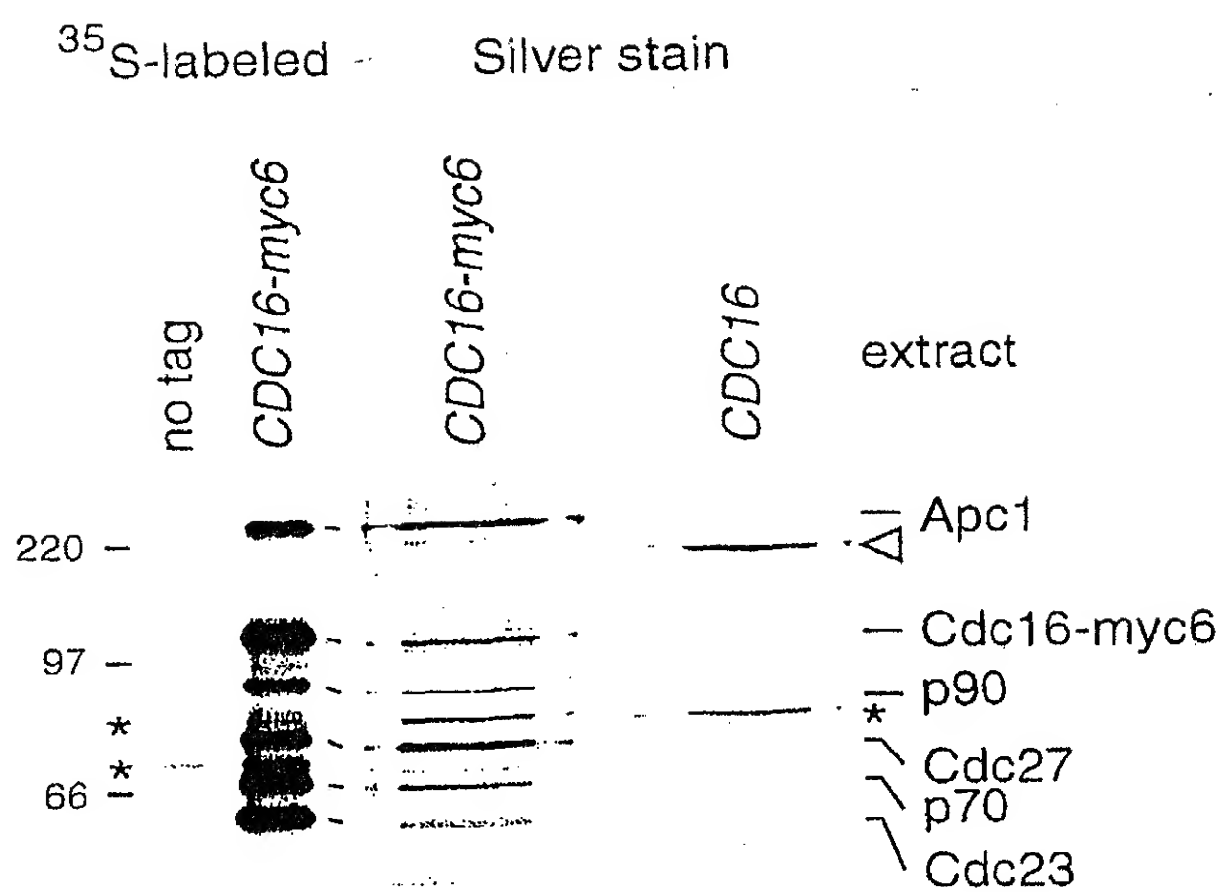
apc1 . . . . . HPLQELHFFWSIAVEPRCLVIKDISTGDAVNNVPIELVVEEDVEKEEVIREISTP 1590  
bime VLONECHLOAERHLUVLAAEPRCIVPRDLDSRRPI. . . SMPITVTD. . . . . DGVSCTLTAP 1816  
tsg24 STDNRYHLOALRHLYVLAAREPRLLVPVDVDTNTEC. . . YALIEVTYKCTQWYEQTKEELMAP 1654  
Consensus - - DN - - - - - HLOALRHLYVLAAREPRCLVP - D - DT - - - - - P - - - - - PIEVT - - - - - E - V - - - - - EL - AP 2026

apc1 CLLPDES KIKSIRVEMHGVEPLEVHFTDYSA. . . SDEFSGGTIIYIORKSE. . . SVFENKAS 1647  
bime CLLPDENRIAKVEVLSPDYHVLVDEDSNPGVREKROQGDOSIYLRRRAT. . . . . YHPTG 1871  
tsg24 TELPELHLLQMKYRGPRYHLLIDLSGEQHLRSILSKDGVLYVKLRAGQLESYKEDPMG 1714  
Consensus CLLPDL - - - - - IE - - - - - KE - E - EVPL - - - - - DE - K - - - - - E - SGD - - - - - LY - - - - - RRA - - - - - S - - - - - ETP - G 2086

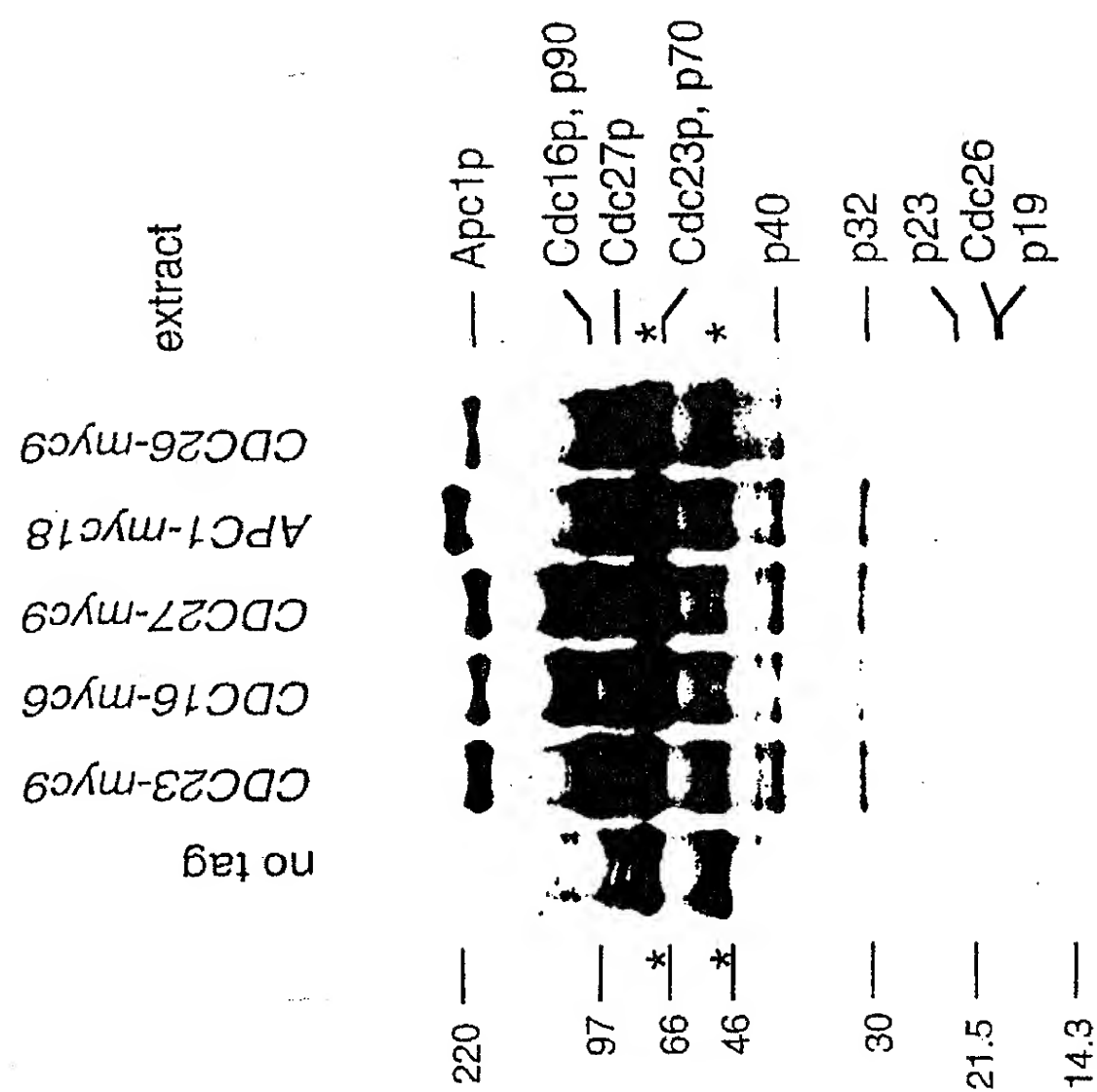
apc1 FRNVEDIHVALKRRKAE. . . SKNYSRLNLKNEQGNNTTSSOLVESLGIQDLTHVELDTLLS 1704  
bime S. . . SFSS. . . TLAGLSSAODILKPASTSSASQKGLSPSALPNVSALES. . . ESHRFTPEPAAQS 1930  
tsg24 WQSLLAQTVAANRNSAARAFKPETISSFT. . . . . SDPALLSFAEYFC. . . EPTVS. . . HGP. . . QEILD 1769  
Consensus - - S - - - - - TVA - - - - - SAA - - - - - S - - - - - S - - - - - N - - - - - S - - - - - AL - - - - - E - L - K - - - - - H - PE - - - - - LS 2146

apc1 AGNNTALT 1713  
bime IWDWIFQL 1939  
tsg24 LFSSIL. . . YE1777  
Consensus - - - - - I - - - - - D2155

**15/22**  
**Fig. 7A**



16/22  
Fig. 7B



B



17/22

Fig. 8

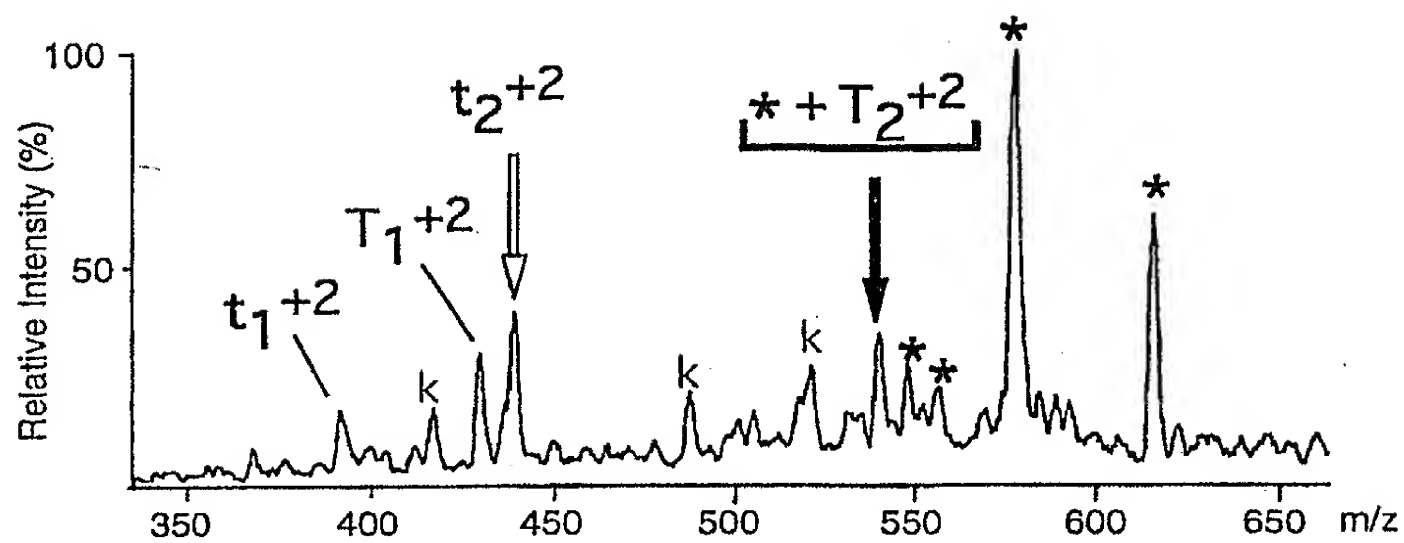
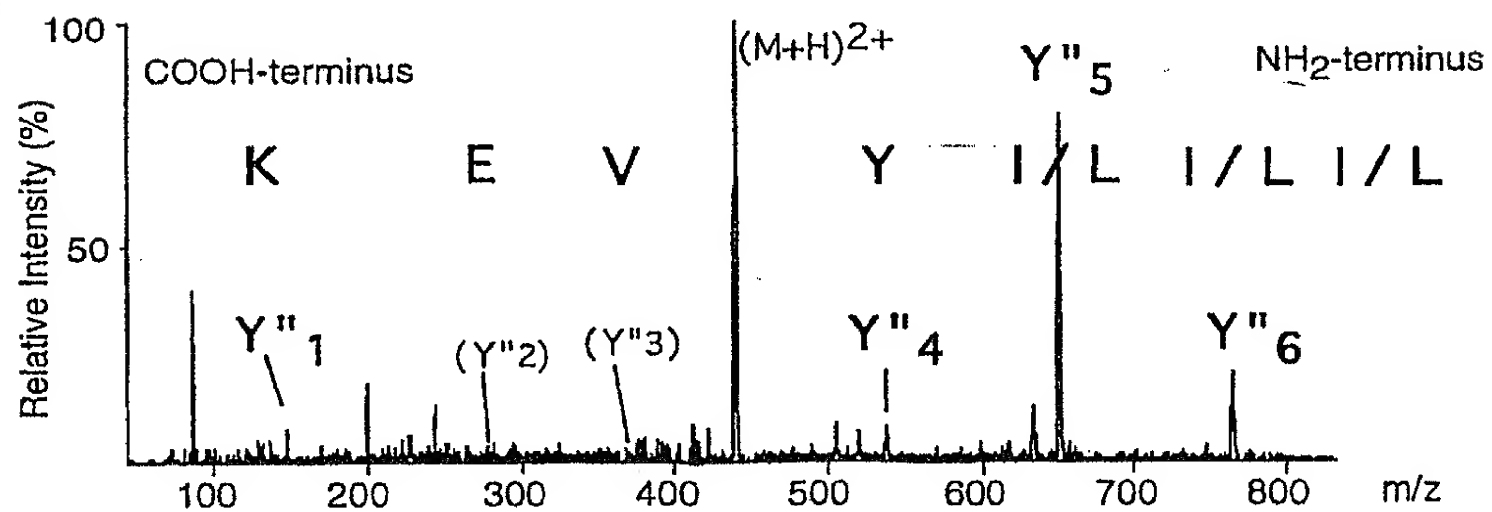
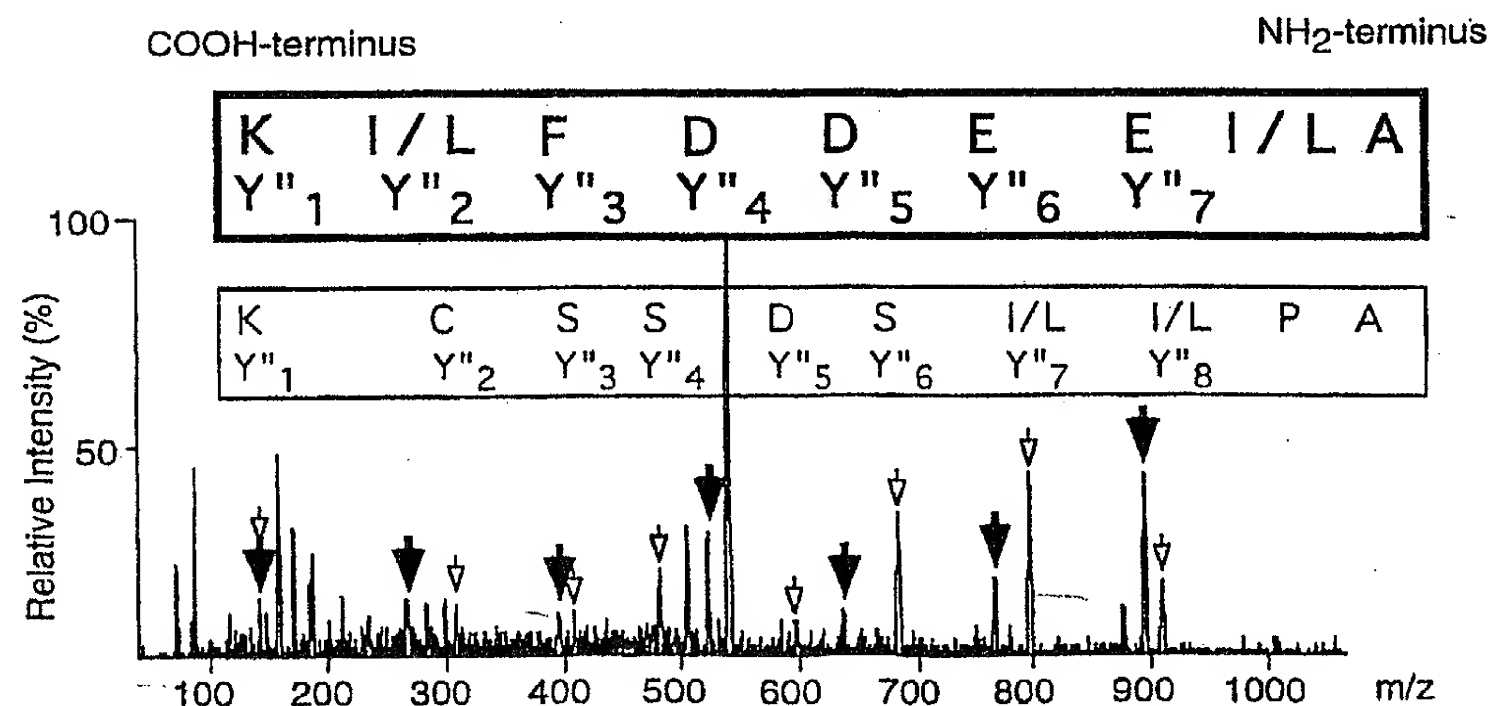
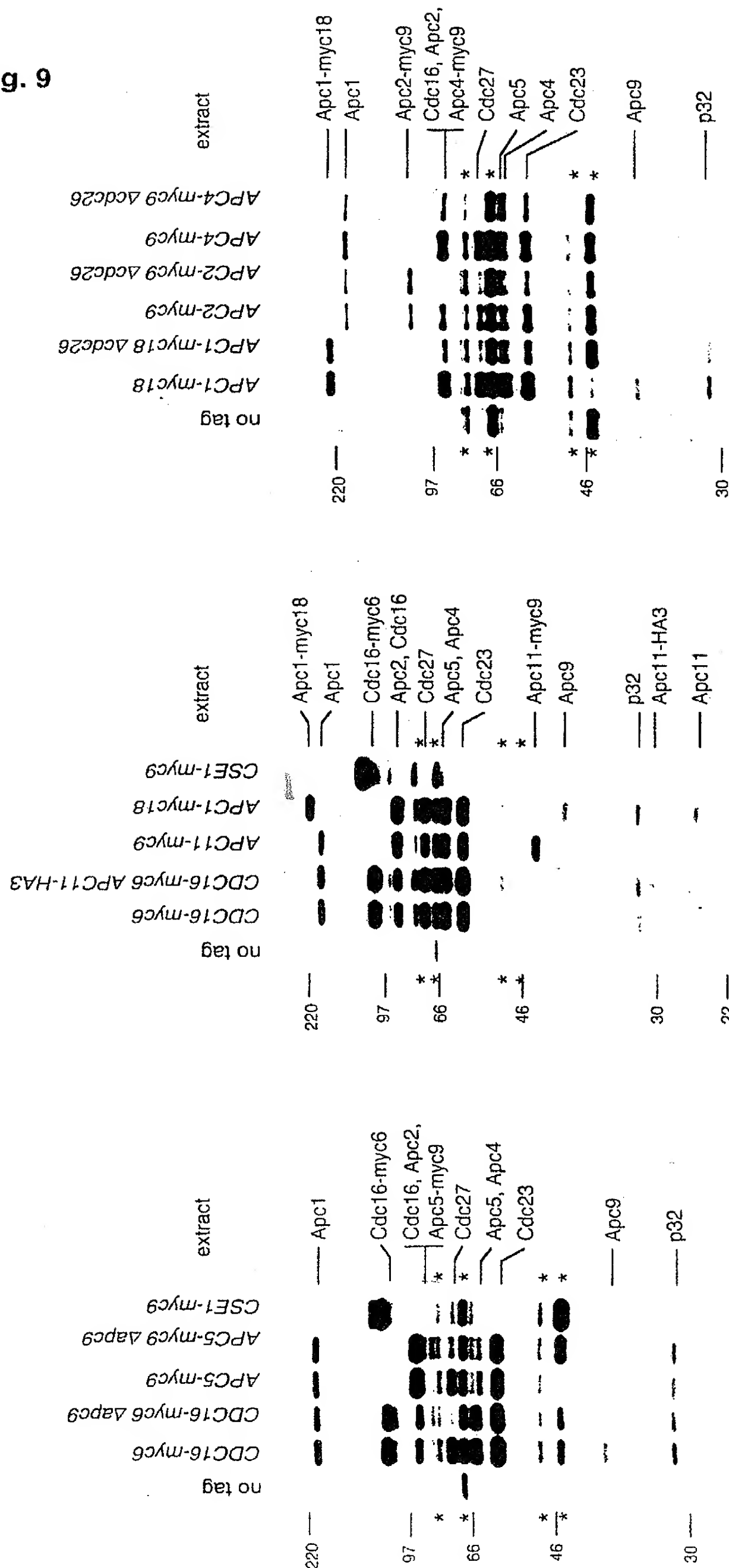
**A****B****C**

Fig. 9

C

B

A



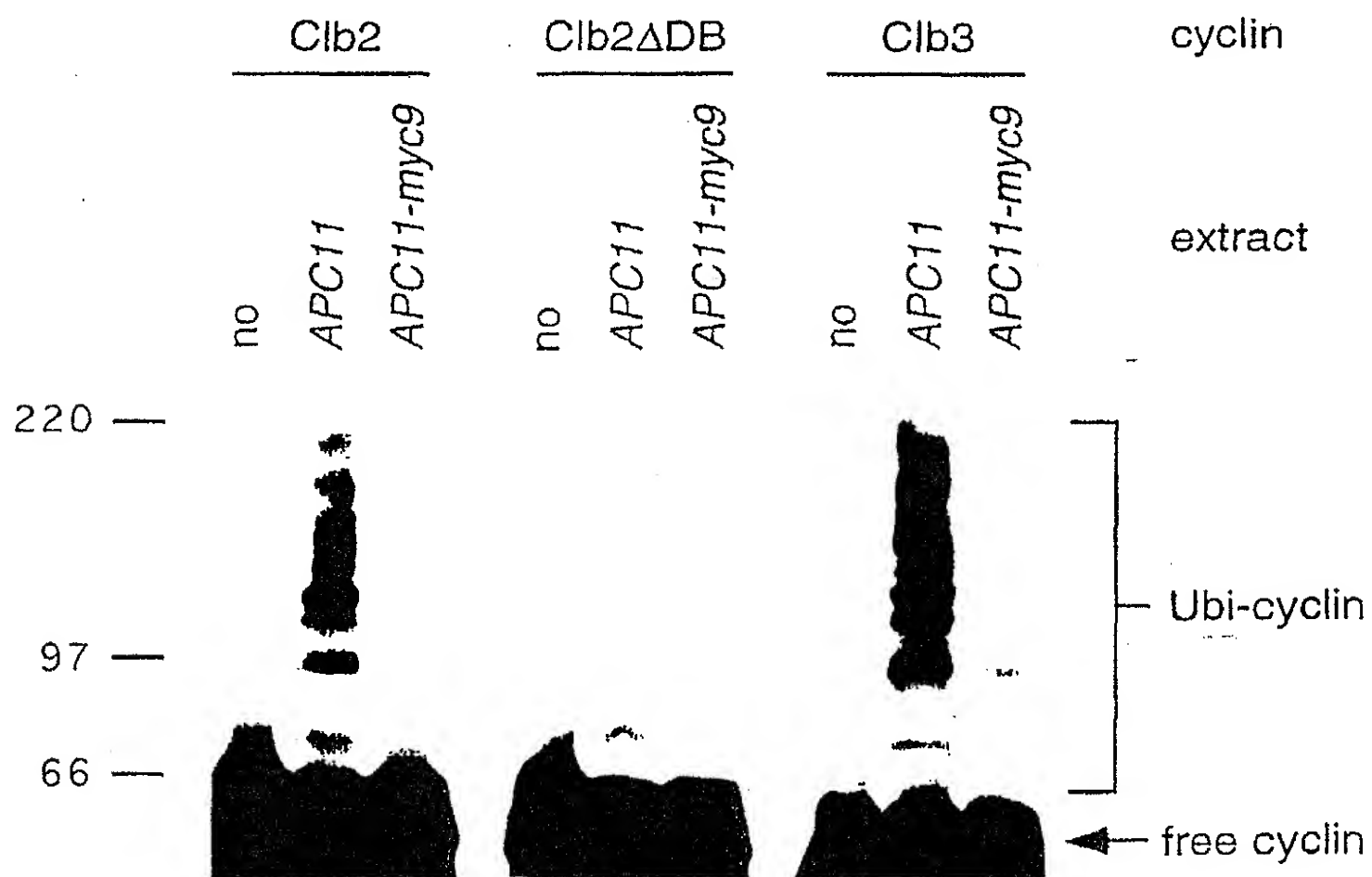
19/22  
Fig. 10

A

Hs M K V K I K C W N G V A T H L H V A N - - - - - D E N C G I C R H A F N G  
Rn M K V K I K C W N G V A T H L H V A N - - - - - D E N C G I C R H A F N G  
Dm M K V T I K S W T G V A T H R H I A N - - - - - D E N C G I C R H S F E S  
Sp M K V K I L R Y H A T A N W S H D T P K - - - - - O D V C G I C R V P F O G  
Sc M X V K I N E V H S V F A W S H I P S T S D E D A A N N O P I G N O E D E D V C G I C R A S Y N G

Hs \* \* \* \*  
Rn C C P D C K V P G D D C P L V H G Q C S H C F H M H C I L K W L N A Q Q V Q D H C P M C R Q E W K F  
Dm C C P E C A L P G D D C P L V H G Q C S H C F H M H C I L K W L N L Q Q P L N K Q C P M C R Q S W K F  
Sp C C P S C T S P G D N C P L V H G K C K H I F H A H C I O N W L A T S G S O G Q C P M C R O T F V V  
Sc C C P S C K F P G D D C P L V T I G L C H H N F H D H C I Y R W L D T P I S K G L C P M C R O T F O L

B



**20/22**  
**Fig. 11A**

A

**Figure 6**

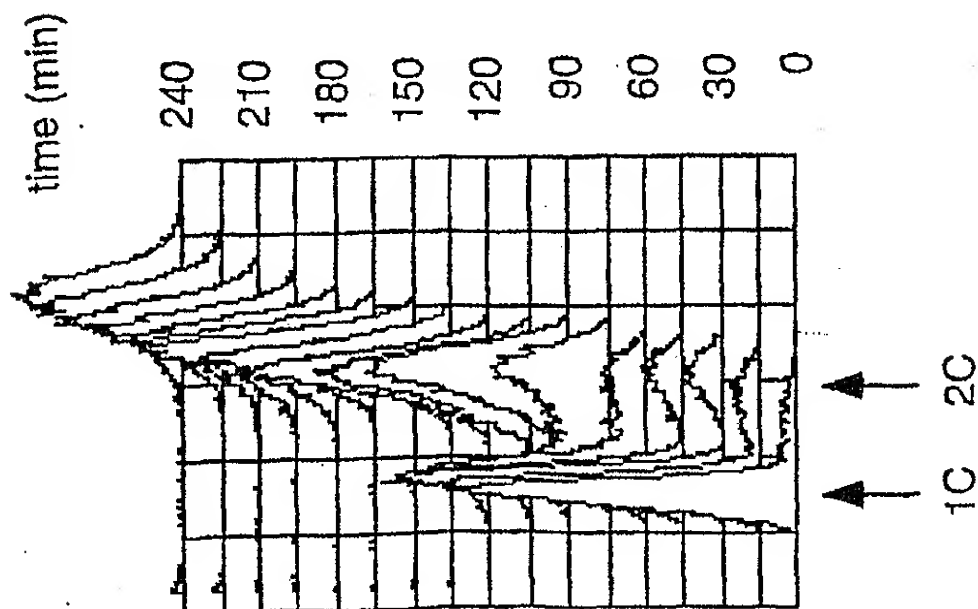
(A) Multiple sequence alignment of the amino acid sequences of Cul proteins from various species. The alignment shows conserved regions across different species, with some residues highlighted in boxes to indicate specific features or mutations.

(B) Multiple sequence alignment of the amino acid sequences of Cul proteins from various species, focusing on a different set of residues compared to panel A.

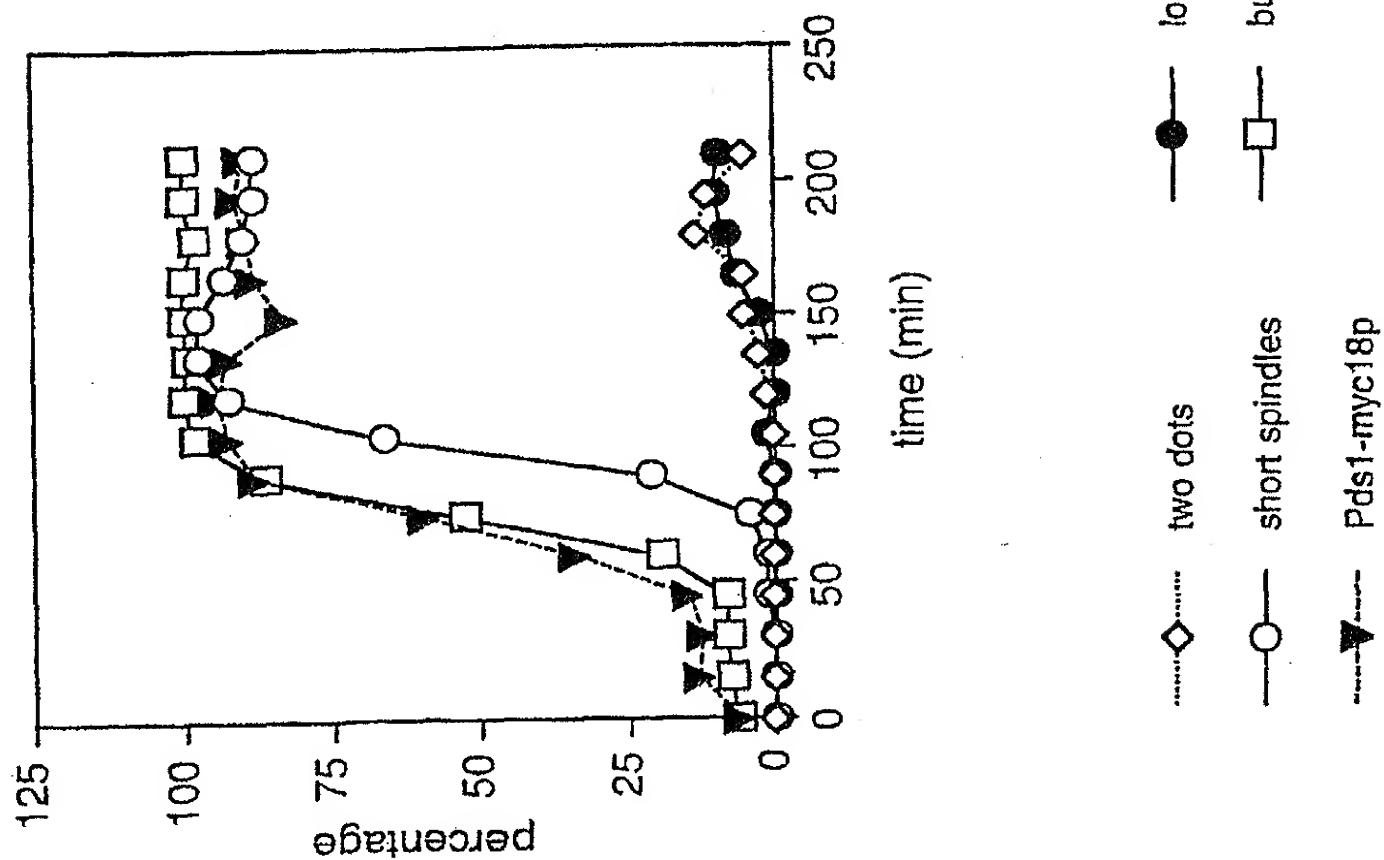
(C) Multiple sequence alignment of the amino acid sequences of Cul proteins from various species, showing another set of conserved regions.

(D) Multiple sequence alignment of the amino acid sequences of Cul proteins from various species, highlighting yet another set of conserved regions.

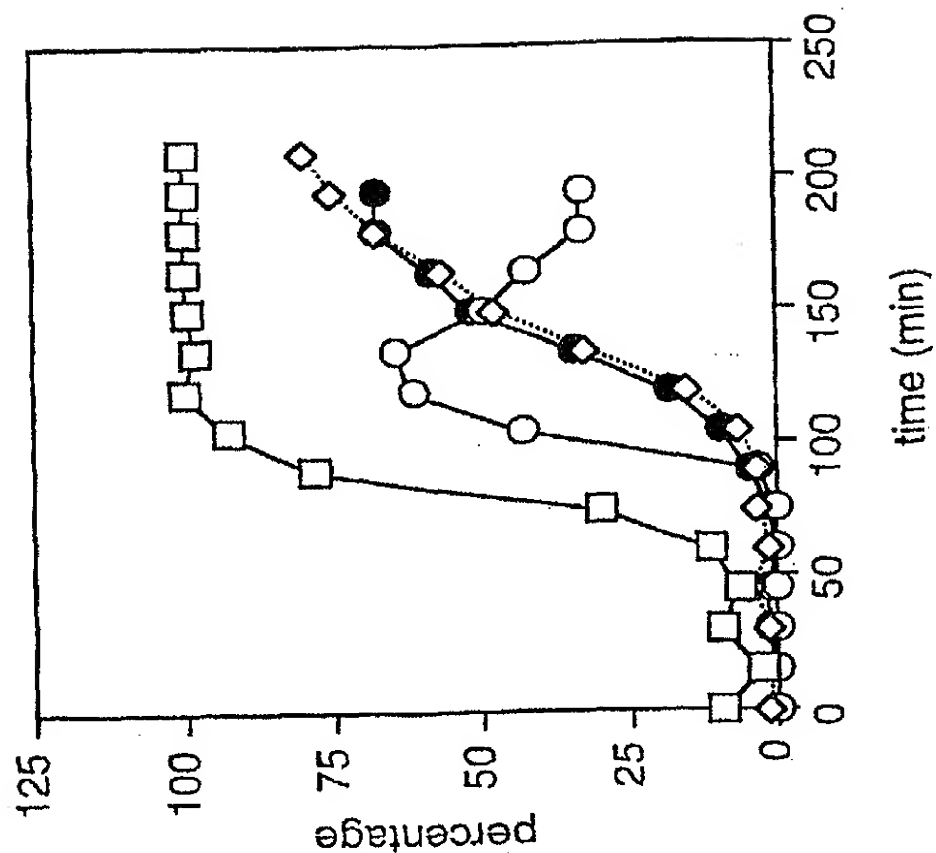
The figure displays four panels (A, B, C, D) of multiple sequence alignments for Cul proteins from various species, including CeCul3, HsCul3, CeCul4, HsCul4a, DmCul1, HsCul1, HsCul2, ScCdc53, CaKOH7.5, MmAp2, and ScAp2. Each panel shows a different segment of the protein sequence, with residues aligned horizontally. Conserved residues are often boxed, and gaps are indicated by dashes (-). Panel A shows the full-length proteins, while panels B, C, and D focus on specific domains or regions of interest.






[illegible][illegible]

apc2-1



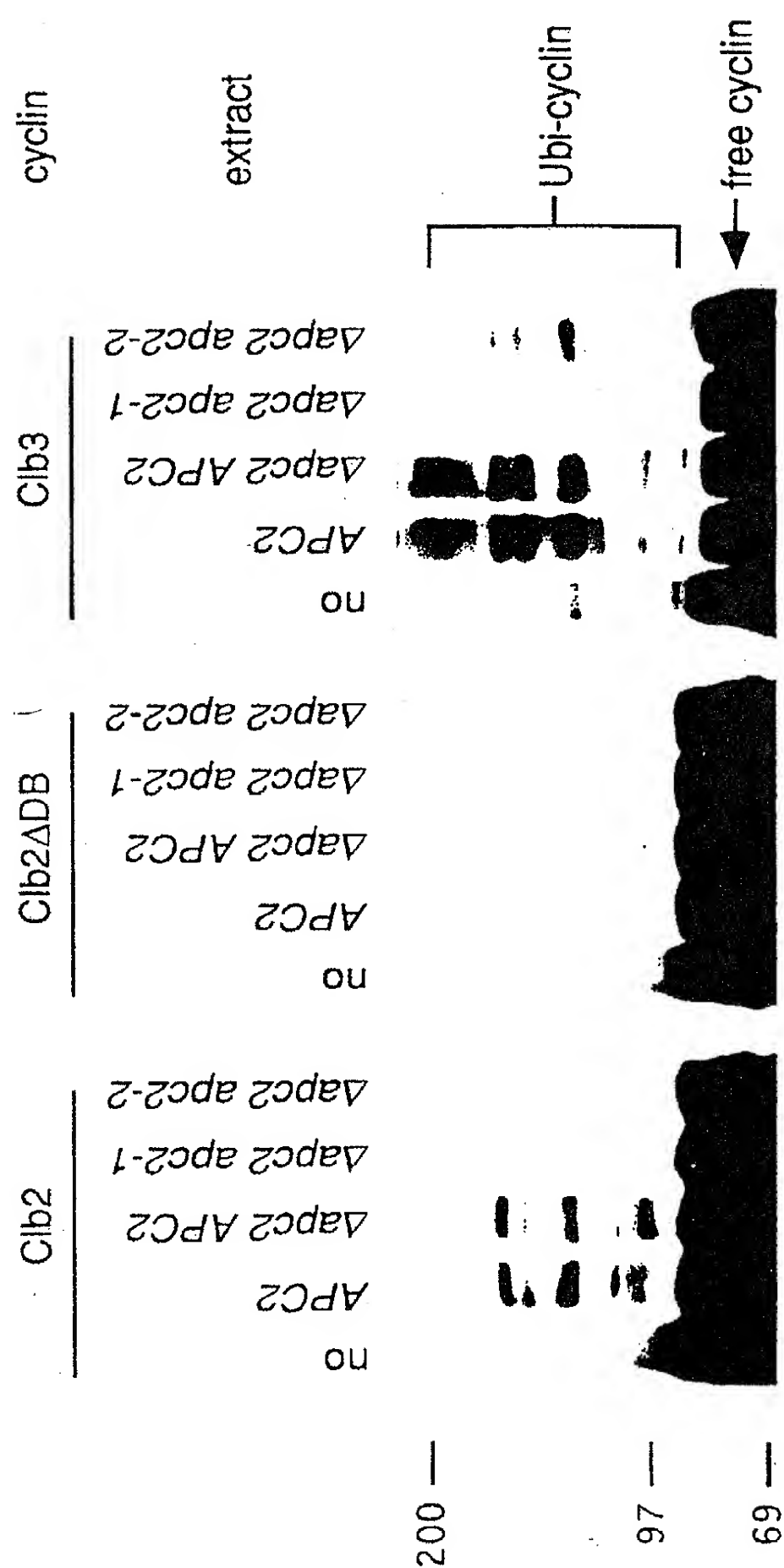
apc2-1 Δpds1



	two dots		long spindles
	short spindles		budded cells
	<i>Pds1-myc18p</i>		

**Fig. 11B**

**22/22**  
**Fig. 11C**



W